

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|---------------------|-------------------|
| | | Match | Length | | | |
| 1 | 311 | 100.0 | 311 | 4 | US-09-634-955B-5 | Sequence 5, Appli |
| 2 | 311 | 100.0 | 311 | 4 | US-09-816-760-5 | Sequence 5, Appli |
| 3 | 311 | 100.0 | 311 | 4 | US-09-838-561-5 | Sequence 5, Appli |
| 4 | 52 | 16.7 | 311 | 4 | US-09-838-561-15 | Sequence 15, Appl |
| 5 | 9 | 2.9 | 682 | 4 | US-09-107-532A-4499 | Sequence 4499, Ap |
| 6 | 9 | 2.9 | 1170 | 4 | US-09-462-136-6 | Sequence 6, Appli |
| 7 | 8 | 2.6 | 113 | 3 | US-08-905-223-439 | Sequence 439, App |
| 8 | 8 | 2.6 | 261 | 4 | US-09-328-352-7731 | Sequence 7731, Ap |
| 9 | 8 | 2.6 | 263 | 4 | US-09-270-767-46093 | Sequence 46093, A |
| 10 | 8 | 2.6 | 299 | 4 | US-09-902-540-14916 | Sequence 14916, A |
| 11 | 8 | 2.6 | 310 | 4 | US-09-907-794A-153 | Sequence 153, App |
| 12 | 8 | 2.6 | 310 | 4 | US-09-905-125A-153 | Sequence 153, App |
| 13 | 8 | 2.6 | 310 | 4 | US-09-902-775A-153 | Sequence 153, App |
| 14 | 8 | 2.6 | 310 | 4 | US-09-906-700-153 | Sequence 153, App |
| 15 | 8 | 2.6 | 310 | 4 | US-09-903-603A-153 | Sequence 153, App |
| 16 | 8 | 2.6 | 310 | 4 | US-09-904-920A-153 | Sequence 153, App |
| 17 | 8 | 2.6 | 310 | 4 | US-09-909-064-153 | Sequence 153, App |

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | Length | DB | ID | Description |
|---------------|-------|------------|--|--------|----|--------------------|-------------------|
| | | Match | | | | | |
| 1 | 1607 | 100.0 | | 311 | 4 | US-09-634-955B-5 | Sequence 5, Appli |
| 2 | 1607 | 100.0 | | 311 | 4 | US-09-816-760-5 | Sequence 5, Appli |
| 3 | 1607 | 100.0 | | 311 | 4 | US-09-838-561-5 | Sequence 5, Appli |
| 4 | 1467 | 91.3 | | 311 | 4 | US-09-838-561-15 | Sequence 15, Appl |
| 5 | 651.5 | 40.5 | | 310 | 4 | US-09-907-794A-153 | Sequence 153, App |
| 6 | 651.5 | 40.5 | | 310 | 4 | US-09-905-125A-153 | Sequence 153, App |
| 7 | 651.5 | 40.5 | | 310 | 4 | US-09-902-775A-153 | Sequence 153, App |
| 8 | 651.5 | 40.5 | | 310 | 4 | US-09-906-700-153 | Sequence 153, App |
| 9 | 651.5 | 40.5 | | 310 | 4 | US-09-903-603A-153 | Sequence 153, App |
| 10 | 651.5 | 40.5 | | 310 | 4 | US-09-904-920A-153 | Sequence 153, App |
| 11 | 651.5 | 40.5 | | 310 | 4 | US-09-909-064-153 | Sequence 153, App |
| 12 | 651.5 | 40.5 | | 310 | 4 | US-09-905-381A-153 | Sequence 153, App |
| 13 | 651.5 | 40.5 | | 310 | 4 | US-09-906-618-153 | Sequence 153, App |

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|-----------|--------------------|
| 1 | 52 | 16.7 | 223 | 2 | Q8CHS7 | Q8chs7 mus musculu |
| 2 | 9 | 2.9 | 281 | 1 | CG11_RAT | P97586 rattus norv |
| 3 | 9 | 2.9 | 1170 | 2 | Q12200 | Q12200 saccharomyc |
| 4 | 8 | 2.6 | 83 | 1 | YORC_TTV1 | P19287 thermoprote |
| 5 | 8 | 2.6 | 134 | 2 | Q89T92 | Q89t92 bradyrhizob |
| 6 | 8 | 2.6 | 137 | 2 | Q6ZTJ1 | Q6ztj1 homo sapien |
| 7 | 8 | 2.6 | 150 | 2 | Q747K4 | Q747k4 geobacter s |
| 8 | 8 | 2.6 | 216 | 2 | Q72RN4 | Q72rn4 leptospira |
| 9 | 8 | 2.6 | 216 | 2 | Q8F428 | Q8f428 leptospira |
| 10 | 8 | 2.6 | 226 | 2 | Q8MT30 | Q8mt30 drosophila |
| 11 | 8 | 2.6 | 233 | 2 | Q9CHT7 | Q9cht7 lactococcus |
| 12 | 8 | 2.6 | 235 | 2 | Q6XHS1 | Q6xhs1 drosophila |
| 13 | 8 | 2.6 | 237 | 2 | Q6IDG8 | Q6idg8 drosophila |
| 14 | 8 | 2.6 | 244 | 2 | Q8D3B0 | Q8d3b0 wiggleswort |

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 9 | 2.9 | 1170 | 2 | S52525 | probable membrane |
| 2 | 8 | 2.6 | 233 | 2 | G86703 | oxidoreductase ygc |
| 3 | 8 | 2.6 | 260 | 2 | E70881 | probable fabG5 pro |
| 4 | 8 | 2.6 | 261 | 2 | G82082 | conserved hypothet |
| 5 | 8 | 2.6 | 262 | 2 | T34378 | hypothetical prote |
| 6 | 8 | 2.6 | 293 | 2 | T19954 | hypothetical prote |
| 7 | 8 | 2.6 | 325 | 2 | T17307 | hypothetical prote |
| 8 | 8 | 2.6 | 341 | 2 | D70761 | probable fatty-acy |
| 9 | 8 | 2.6 | 371 | 2 | A44122 | alpha-helical coil |
| 10 | 8 | 2.6 | 938 | 2 | T34105 | hypothetical prote |
| 11 | 8 | 2.6 | 964 | 2 | AG3433 | diguanylate cyclas |
| 12 | 7 | 2.3 | 135 | 2 | G89751 | protein C33E10.10 |
| 13 | 7 | 2.3 | 141 | 2 | C97338 | hydroxymyristoyl-(|
| 14 | 7 | 2.3 | 146 | 2 | G97030 | probable membrane |
| 15 | 7 | 2.3 | 148 | 2 | F86899 | hypothetical prote |
| 16 | 7 | 2.3 | 151 | 2 | D75347 | hypothetical prote |
| 17 | 7 | 2.3 | 157 | 2 | C71477 | probable ribityllu |
| 18 | 7 | 2.3 | 167 | 2 | D82561 | probable signal pe |
| 19 | 7 | 2.3 | 184 | 2 | B72601 | hypothetical prote |
| 20 | 7 | 2.3 | 198 | 2 | B82080 | flavodoxin [simila |
| 21 | 7 | 2.3 | 200 | 2 | T42066 | glutamate-ammonia |

Database : PIR_79:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | Length | DB | ID | Description |
|---------------|-------|------------|--|--------|----|--------|--------------------|
| | | Match | | | | | |
| 1 | 640.5 | 39.9 | | 325 | 2 | T17307 | hypothetical prote |
| 2 | 311.5 | 19.4 | | 537 | 2 | T34380 | hypothetical prote |
| 3 | 307 | 19.1 | | 262 | 2 | T34378 | hypothetical prote |
| 4 | 299.5 | 18.6 | | 278 | 2 | E83152 | probable short-cha |
| 5 | 274 | 17.1 | | 277 | 2 | AG1983 | hypothetical prote |
| 6 | 265.5 | 16.5 | | 263 | 2 | AI1692 | oxidoreductase hom |
| 7 | 265.5 | 16.5 | | 266 | 2 | H97309 | short-chain alcoho |
| 8 | 255.5 | 15.9 | | 263 | 2 | AH1321 | oxidoreductase hom |
| 9 | 253 | 15.7 | | 259 | 2 | A69965 | ketoacyl reductase |
| 10 | 249 | 15.5 | | 259 | 2 | B83838 | oxidoreductase BH1 |
| 11 | 245 | 15.2 | | 293 | 2 | AD2176 | oxidoreductase all |
| 12 | 242 | 15.1 | | 270 | 2 | E86788 | oxidoreductase yne |
| 13 | 241.5 | 15.0 | | 328 | 2 | F75374 | probable ketoacyl |
| 14 | 241 | 15.0 | | 247 | 2 | F90254 | hypothetical prote |
| 15 | 241 | 15.0 | | 253 | 2 | A95223 | hypothetical prote |
| 16 | 238.5 | 14.8 | | 287 | 2 | C55210 | hetN protein - Ana |
| 17 | 235.5 | 14.7 | | 287 | 2 | AF2475 | ketoacyl reductase |
| 18 | 234.5 | 14.6 | | 307 | 2 | E70082 | glucose 1-dehydrog |
| 19 | 234 | 14.6 | | 261 | 1 | A28788 | actinorhodin polyk |
| 20 | 233 | 14.5 | | 332 | 2 | S37652 | follicular lymphom |

OM protein - protein search, using sw model

Run on: March 12, 2005, 13:06:08 ; Search time 174 Seconds
(without alignments)
915.268 Million cell updates/sec

Title: US-10-664-506-5
Perfect score: 1607
Sequence: 1 MGVMAMLMPLLLLLGISGLL.....FFFAVVACGVKEKLNVP EEG 311

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|--------|--------------------|
| 1 | 1017 | 63.3 | 223 | 2 | Q8CHS7 | Q8chs7 mus musculu |
| 2 | 651.5 | 40.5 | 310 | 2 | Q6UX59 | Q6ux59 homo sapien |
| 3 | 651.5 | 40.5 | 325 | 2 | Q9BTF9 | Q9btf9 homo sapien |
| 4 | 650.5 | 40.5 | 325 | 2 | Q6IAN0 | Q6ian0 homo sapien |
| 5 | 640.5 | 39.9 | 325 | 2 | Q9UFM6 | Q9ufm6 homo sapien |
| 6 | 625.5 | 38.9 | 323 | 2 | Q99J47 | Q99j47 m similar t |
| 7 | 557 | 34.7 | 291 | 2 | Q9Y3A1 | Q9y3a1 homo sapien |
| 8 | 466 | 29.0 | 326 | 2 | Q9Y140 | Q9y140 drosophila |
| 9 | 458 | 28.5 | 317 | 2 | Q7Q732 | Q7q732 anopheles g |
| 10 | 331 | 20.6 | 311 | 2 | Q65ZI3 | Q65zi3 caenorhabdi |
| 11 | 322 | 20.0 | 264 | 2 | Q81M93 | Q81m93 bacillus an |
| 12 | 321 | 20.0 | 264 | 2 | Q635E8 | Q635e8 bacillus ce |
| 13 | 320 | 19.9 | 264 | 2 | Q731G1 | Q731g1 bacillus ce |
| 14 | 311.5 | 19.4 | 537 | 2 | Q22787 | Q22787 caenorhabdi |
| 15 | 309 | 19.2 | 264 | 2 | Q6HE26 | Q6he26 bacillus th |

| | | | | | | | |
|----|-------|------|-----|---|------------|--------|-------------|
| 16 | 302.5 | 18.8 | 268 | 2 | Q6F8F2 | Q6f8f2 | acinetobact |
| 17 | 299.5 | 18.6 | 278 | 2 | Q9HX59 | Q9hx59 | pseudomonas |
| 18 | 295.5 | 18.4 | 339 | 1 | DHS7_HUMAN | Q9y394 | homo sapien |
| 19 | 295.5 | 18.4 | 375 | 2 | Q659E8 | Q659e8 | homo sapien |
| 20 | 290.5 | 18.1 | 267 | 2 | Q8EJM5 | Q8ejm5 | shewanella |
| 21 | 288.5 | 18.0 | 324 | 2 | Q6I7R1 | Q6i7r1 | rattus norv |
| 22 | 286.5 | 17.8 | 260 | 2 | O15744 | O15744 | dictyosteli |
| 23 | 282 | 17.5 | 338 | 1 | DHS7_MOUSE | Q9cxr1 | mus musculu |
| 24 | 277 | 17.2 | 273 | 2 | Q6W1F0 | Q6w1f0 | rhizobium s |
| 25 | 276 | 17.2 | 336 | 2 | Q6GP08 | Q6gp08 | xenopus lae |
| 26 | 274 | 17.1 | 277 | 2 | Q8YX01 | Q8yx01 | anabaena sp |
| 27 | 271 | 16.9 | 268 | 2 | Q6CNU5 | Q6cnu5 | kluveromyc |
| 28 | 265.5 | 16.5 | 263 | 2 | Q92A39 | Q92a39 | listeria in |
| 29 | 265.5 | 16.5 | 266 | 2 | Q97DY5 | Q97dy5 | clostridium |
| 30 | 263 | 16.4 | 298 | 2 | Q87XV8 | Q87xv8 | pseudomonas |
| 31 | 262.5 | 16.3 | 260 | 2 | Q65HP3 | Q65hp3 | bacillus li |
| 32 | 260.5 | 16.2 | 263 | 2 | Q71Y45 | Q71y45 | listeria mo |
| 33 | 258 | 16.1 | 312 | 2 | Q9N126 | Q9n126 | bos taurus |
| 34 | 258 | 16.1 | 316 | 2 | Q8T197 | Q8t197 | dictyosteli |
| 35 | 256 | 15.9 | 280 | 2 | Q65F58 | Q65f58 | bacillus li |
| 36 | 255.5 | 15.9 | 248 | 2 | Q9RH22 | Q9rh22 | zymomonas m |
| 37 | 255.5 | 15.9 | 263 | 2 | Q8Y5S9 | Q8y5s9 | listeria mo |
| 38 | 254 | 15.8 | 303 | 2 | Q6F7B8 | Q6f7b8 | acinetobact |
| 39 | 253 | 15.7 | 259 | 1 | YQJQ_BACSU | P54554 | bacillus su |
| 40 | 253 | 15.7 | 295 | 2 | Q8RR58 | Q8rr58 | acinetobact |
| 41 | 252 | 15.7 | 295 | 2 | P94129 | P94129 | acinetobact |
| 42 | 250.5 | 15.6 | 271 | 2 | Q7UPD8 | Q7upd8 | rhodopirell |
| 43 | 249.5 | 15.5 | 311 | 2 | Q9NYR8 | Q9nyr8 | homo sapien |
| 44 | 249 | 15.5 | 259 | 2 | Q9KCR3 | Q9kcr3 | bacillus ha |
| 45 | 247 | 15.4 | 276 | 2 | Q9ALU7 | Q9alu7 | enterobacte |

ALIGNMENTS

RESULT 1

Q8CHS7

ID Q8CHS7 PRELIMINARY; PRT; 223 AA.
AC Q8CHS7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to CGI-86-protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,


```

      |||  ||||: |||||  |||||:|:|: :| :|  | :  |:
Db      181 QGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGS- 239

Qy      237 EASIWKFFFRKLTYGV-----HPVEVAEEVMRTVRRKKQEVFMANPIPKAAVYVRT 287
      |||  ||||:|:|  | :||:| :|: :|  |||:|
Db      240 -----RYGVMDTTTAQGRSPVEVAQDVLAAVGKKKKDVLADLLPSLAVYLRT 287

Qy      288 FFPEFFFAVVACGVKEK 304
      |  ||:|  :|
Db      288 LAPGLFFSLMASRARKE 304

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RESULT 3

Q9BTF9

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ID      Q9BTF9          PRELIMINARY;          PRT;          325 AA.
AC      Q9BTF9;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      DKFZP5660084 protein.
GN      Name=DKFZp5660084;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RA      Strausberg R.;
RL      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;

```

Database : A_Geneseq_16Dec04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % | | DB | ID | Description |
|---------------|-------|----------------|--------|----|----------|--------------------|
| | | Query Match | Length | | | |
| 1 | 311 | 100.0 | 311 | 4 | AAB47593 | Aab47593 Human DHD |
| 2 | 311 | 100.0 | 311 | 6 | ABP58046 | Abp58046 Human deh |
| 3 | 311 | 100.0 | 311 | 8 | ADG40199 | Adg40199 Human deh |
| 4 | 255 | 82.0 | 311 | 3 | AAB08911 | Aab08911 Human sec |
| 5 | 255 | 82.0 | 345 | 3 | AAB08948 | Aab08948 Human sec |
| 6 | 156 | 50.2 | 246 | 8 | ADM33425 | Adm33425 Human PRO |
| 7 | 107 | 34.4 | 118 | 4 | AAM24151 | Aam24151 Human EST |
| 8 | 70 | 22.5 | 81 | 8 | ABO54789 | Abo54789 Human gen |
| 9 | 52 | 16.7 | 311 | 6 | ABP58047 | Abp58047 Mouse deh |
| 10 | 52 | 16.7 | 311 | 8 | ADG40201 | Adg40201 Mouse deh |
| 11 | 29 | 9.3 | 29 | 3 | AAB08949 | Aab08949 Human sec |
| 12 | 9 | 2.9 | 31 | 6 | ADA98202 | Ada98202 Human sec |
| 13 | 9 | 2.9 | 31 | 6 | ADA44050 | Ada44050 Human sec |
| 14 | 9 | 2.9 | 31 | 7 | ADC20368 | Adc20368 Human sec |
| 15 | 9 | 2.9 | 31 | 7 | ADF10701 | Adf10701 Human sec |
| 16 | 9 | 2.9 | 32 | 4 | AAB60717 | Aab60717 Human sec |
| 17 | 9 | 2.9 | 281 | 2 | AAW38423 | Aaw38423 Rat cell |
| 18 | 9 | 2.9 | 281 | 7 | ADE62861 | Ade62861 Rat Prote |

RESULT 4

AAB08911

ID AAB08911 standard; protein; 311 AA.

XX

AC AAB08911;

XX

DT 30-AUG-2000 (first entry)

XX

DE Human secreted protein sequence encoded by gene 21 SEQ ID NO:68.

XX

KW Human; secreted protein; cytostatic; anti-proliferative; vulnerary;
KW immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;
KW hyperproliferative disorder; infectious disease; tissue regeneration;
KW screening; food additive; preservative; wound healing;
KW hyper-vascular disease; chromosome 11.

XX

OS Homo sapiens.

XX

PN WO200017222-A1.

XX

PD 30-MAR-2000.

XX

PF 22-SEP-1999; 99WO-US022012.

XX

PR 23-SEP-1998; 98US-0101546P.

PR 02-OCT-1998; 98US-0102895P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;
PI Komatsoulis G, Endress GA, Soppet DR;

XX

DR WPI; 2000-283538/24.

DR N-PSDB; AAA39072.

XX

PT Human secreted proteins and coding sequences useful in diagnostic and
PT therapeutic methods for disorders such as immune system or proliferative
PT disorders, related to the proteins.

XX

PS Claim 11; Page 366-367; 416pp; English.

XX

CC The polynucleotide sequences given in AAA39052 to AAA39088 encode the
CC human secreted proteins given in AAB08891 to AAB08984. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic; anti-
CC proliferative; immunosuppressive; antibacterial; and vulnerary. The
CC secreted proteins and their related polynucleotide sequences are useful
CC for diagnostic and therapeutic methods useful for diagnosing and treating
CC disorders related to the secreted proteins. The proteins, and
CC polynucleotide sequences may be useful for treating disorders of the
CC immune system, hyperproliferative disorders, infectious disease,
CC regeneration of tissues, for chemotaxis and for screening molecules that
CC bind to the proteins. The proteins or polynucleotide sequences may be
CC used as food additives or preservatives, to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, co-factors or other nutritional components. Agonists or
CC antagonists of the proteins may be used to prevent scar tissue growth

CC during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051
CC and AAB08890 are sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 311 AA;

Query Match 82.0%; Score 255; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 2e-231;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 1 | MGVMAMLMPLLLLLGISGLLFIYQEVSRWSKSAVQNKVVVITDAISGLGKECARVFHTG | 60 |
| | | | |
| Db | 1 | MGVMAMLMPLLLLLGISGLLFIYQEVSRWSKSAVQNKVVVITDAISGLGKECARVFHTG | 60 |
| Qy | 61 | GARLVLCGKNWERLENLYDALISVADPSKTFTPKLVLLDLSDISCVPDVAKEVLDCYGCV | 120 |
| | | | |
| Db | 61 | GARLVLCGKNWERLENLYDALISVADPSKTFTPKLVLLDLSDISCVPDVAKEVLDCYGCV | 120 |
| Qy | 121 | DILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTKALLPNMISRRTGQIVLVNNIQ | 180 |
| | | | |
| Db | 121 | DILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTKALLPNMISRRTGQIVLVNNIQ | 180 |
| Qy | 181 | GKFGIPFRTTYAASKHAALGFFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASI | 240 |
| | | | |
| Db | 181 | GKFGIPFRTTYAASKHAALGFFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASI | 240 |
| Qy | 241 | WKFFFRKLTYGVHPV | 255 |
| | | | |
| Db | 241 | WKFFFRKLTYGVHPV | 255 |

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-------------------|-------------------|
| 1 | 311 | 100.0 | 311 | 9 | US-09-838-561-5 | Sequence 5, Appli |
| 2 | 311 | 100.0 | 311 | 9 | US-09-816-760-5 | Sequence 5, Appli |
| 3 | 311 | 100.0 | 311 | 14 | US-10-172-585-5 | Sequence 5, Appli |
| 4 | 311 | 100.0 | 311 | 15 | US-10-144-433-2 | Sequence 2, Appli |
| 5 | 311 | 100.0 | 311 | 15 | US-10-664-506-5 | Sequence 5, Appli |
| 6 | 311 | 100.0 | 311 | 15 | US-10-144-433-2 | Sequence 2, Appli |
| 7 | 255 | 82.0 | 311 | 9 | US-09-820-893-68 | Sequence 68, Appl |
| 8 | 255 | 82.0 | 311 | 15 | US-10-607-565-68 | Sequence 68, Appl |
| 9 | 255 | 82.0 | 345 | 9 | US-09-820-893-106 | Sequence 106, App |
| 10 | 255 | 82.0 | 345 | 15 | US-10-607-565-106 | Sequence 106, App |

AI091419/c

DEFINITION [ow62e03.x1](#) Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651420 3' similar to WP:T25G12.7 CE07544 DEHYDROGENASE ;contains TAR1.t3 MER22 repetitive element ;, mRNA sequence.

VERSION AI091419.1 GI:3430478

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cqapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1044 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 453.

FEATURES Location/Qualifiers

```
source      1.  .631
```

```
/organism="Homo sapiens"
```

```
/mol type="mRNA"
```

```
/db xref="taxon:9606"
```

```
/clone="IMAGE:1651420"
```

```
/lab host="DH10B"
```

```
/clone lib="Soares NSF F8 9W OT PA P S1"
```

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1:

309384-310919_323208-325895_Soares_Nb2HP pool 1:

145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares Nb2HF8-9W pool 1:

758280-760583, 772104-774407 Soares NbHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NbHOT

pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

Query Match 45.0%; Score 621; DB 1; Length 631;

Best Local Similarity 100.0%; Pred. No. 5.9e-294;

Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 698 TCATCAACAATGCCAGTGTGAAGGTGAAGGGGCCTGCCATAAGATTTCTCTGGAGCTCG 757

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 5 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|

| | | | |
|----|------|---------------------------------------------------------------|------|
| Db | 621 | TCATCAACAATGCCAGTGTGAAGGTGAAGGGGCCTGCCCATAGATTTCTCTGGAGCTCG | 562 |
| Qy | 758 | ACAAAAAGATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTC | 817 |
| | | | |
| Db | 561 | ACAAAAAGATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTC | 502 |
| Qy | 818 | CCAACATGATCTCCCGGAGAAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGT | 877 |
| | | | |
| Db | 501 | CCAACATGATCTCCCGGAGAAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGT | 442 |
| Qy | 878 | TTGGAATCCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTG | 937 |
| | | | |
| Db | 441 | TTGGAATCCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTG | 382 |
| Qy | 938 | ACTGCCTCCGAGCCGAAGTGGAGGAATACGATGTTGTTCATCAGCACCGTGAGCCCGACTT | 997 |
| | | | |
| Db | 381 | ACTGCCTCCGAGCCGAAGTGGAGGAATACGATGTTGTTCATCAGCACCGTGAGCCCGACTT | 322 |
| Qy | 998 | TCATCCGGTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTTGGAAAT | 1057 |
| | | | |
| Db | 321 | TCATCCGGTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTTGGAAAT | 262 |
| Qy | 1058 | TCTTTTTCAGGAAGCTGACCTACGGCGTGCACCCAGTAGAGGTGGCGGAGGAGGTGATGC | 1117 |
| | | | |
| Db | 261 | TCTTTTTCAGGAAGCTGACCTACGGCGTGCACCCAGTAGAGGTGGCGGAGGAGGTGATGC | 202 |
| Qy | 1118 | GCACCGTGCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCG | 1177 |
| | | | |
| Db | 201 | GCACCGTGCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCG | 142 |
| Qy | 1178 | TGTACGTCCGCACCTTCTTCCCGAGTTCTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGG | 1237 |
| | | | |
| Db | 141 | TGTACGTCCGCACCTTCTTCCCGAGTTCTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGG | 82 |
| Qy | 1238 | AGAAGCTCAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGGCCACCCCTTGGA | 1297 |
| | | | |
| Db | 81 | AGAAGCTCAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGGCCACCCCTTGGA | 22 |
| Qy | 1298 | AATAAAGGTTTTTCTGGCAAA | 1318 |
| | | | |
| Db | 21 | AATAAAGGTTTTTCTGGCAAA | 1 |

RESULT 2
 AI741629/c
 LOCUS AI741629 632 bp mRNA linear EST 19-DEC-1999
 DEFINITION wg28f07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:2366437 3' similar to WP:T25G12.7 CE07544 DEHYDROGENASE
 ;contains TAR1.t3 MER22 repetitive element ;; mRNA sequence.
 ACCESSION AI741629
 VERSION AI741629.1 GI:5109917
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 632)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1035 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 444.
 FEATURES Location/Qualifiers
 source 1..632
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2366437"
 /lab_host="DH10B"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and cloneIDs: Soares NbHSF pool 1:
 309384-310919, 323208-325895 Soares Nb2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares Nb2HF8-9W pool 1:
 758280-760583, 772104-774407 Soares NbHPA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NbHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 40.0%; Score 551; DB 1; Length 632;
 Best Local Similarity 99.8%; Pred. No. 1.7e-259;
 Matches 601; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 705 CAATGCCAGTGTGAAGGTGAAGGGCCTGCCCATAGATTCTCTGGAGCTCGACAAAAA 764
 |||

| | | | |
|----|------|---------------------------------------------------------------|------|
| Db | 615 | CAATGCCAGTGTGAAGGTGAAGGGGCTGCCCATAGATTCTCTGGAGCTCGACAGAAA | 556 |
| Qy | 765 | GATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTCCCAACAT | 824 |
| | | | |
| Db | 555 | GATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTCCCAACAT | 496 |
| Qy | 825 | GATCTCCCGGAGAAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGTTTGGAAT | 884 |
| | | | |
| Db | 495 | GATCTCCCGGAGAAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGTTTGGAAT | 436 |
| Qy | 885 | CCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTGACTGCCT | 944 |
| | | | |
| Db | 435 | CCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTGACTGCCT | 376 |
| Qy | 945 | CCGAGCCGAAGTGGAGGAATACGATGTTGTCATCAGCACCGTGAGCCCGACTTTTCATCCG | 1004 |
| | | | |
| Db | 375 | CCGAGCCGAAGTGGAGGAATACGATGTTGTCATCAGCACCGTGAGCCCGACTTTTCATCCG | 316 |
| Qy | 1005 | GTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTTGGAAATTCTTTTT | 1064 |
| | | | |
| Db | 315 | GTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTTGGAAATTCTTTTT | 256 |
| Qy | 1065 | CAGGAAGCTGACCTACGGCGTGACCCAGTAGAGGTGGCGGAGGAGGTGATGCGCACCGT | 1124 |
| | | | |
| Db | 255 | CAGGAAGCTGACCTACGGCGTGACCCAGTAGAGGTGGCGGAGGAGGTGATGCGCACCGT | 196 |
| Qy | 1125 | GCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCGTGTACGT | 1184 |
| | | | |
| Db | 195 | GCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCGTGTACGT | 136 |
| Qy | 1185 | CCGCACCTTCTTCCCGAGTTCTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGGAGAAGCT | 1244 |
| | | | |
| Db | 135 | CCGCACCTTCTTCCCGAGTTCTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGGAGAAGCT | 76 |
| Qy | 1245 | CAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGCCACCCCTTGGAAATAAAG | 1304 |
| | | | |
| Db | 75 | CAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGCCACCCCTTGGAAATAAAG | 16 |
| Qy | 1305 | GT | 1306 |
| | | | |
| Db | 15 | GT | 14 |

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % Query | | Length | DB | ID | Description |
|---------------|------------|-------|--------|----|----------|--------------------|
| | Score | Match | | | | |
| 1 | 1379 | 100.0 | 1379 | 4 | AAH43561 | Aah43561 Human DHD |
| 2 | 1379 | 100.0 | 1379 | 10 | ABV76050 | Abv76050 Human deh |
| 3 | 1379 | 100.0 | 1379 | 12 | ADG40198 | Adg40198 cDNA enco |
| 4 | 1004 | 72.8 | 1114 | 8 | ABX71069 | Abx71069 Novel hum |
| 5 | 955 | 69.3 | 1157 | 3 | AAA39072 | Aaa39072 Human sec |
| 6 | 936 | 67.9 | 936 | 4 | AAH43565 | Aah43565 Human DHD |
| 7 | 677 | 49.1 | 797 | 12 | ADM33424 | Adm33424 Human PRO |
| 8 | 327 | 23.7 | 780 | 4 | AAH98810 | Aah98810 Human EST |
| 9 | 208 | 15.1 | 247 | 12 | ACH82344 | Ach82344 Human gen |
| 10 | 208 | 15.1 | 514 | 12 | ACH68644 | Ach68644 Human gen |
| c 11 | 159 | 11.5 | 599 | 12 | ACH69248 | Ach69248 Human gen |

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | Query | | | | |
|--------|-------|-------|--------|----|----------|--------------------|--|
| No. | Score | Match | Length | DB | ID | Description | |
| 1 | 1379 | 100.0 | 1379 | 6 | AR278046 | AR278046 Sequence | |
| 2 | 1379 | 100.0 | 1379 | 6 | AR392052 | AR392052 Sequence | |
| 3 | 1379 | 100.0 | 1379 | 6 | AR403912 | AR403912 Sequence | |
| 4 | 1379 | 100.0 | 1379 | 6 | AX320639 | AX320639 Sequence | |
| 5 | 1004 | 72.8 | 1114 | 6 | AR542048 | AR542048 Sequence | |
| 6 | 955 | 69.3 | 1157 | 6 | BD233739 | BD233739 31 human | |
| 7 | 933 | 67.7 | 933 | 6 | AR278047 | AR278047 Sequence | |
| 8 | 933 | 67.7 | 933 | 6 | AR392053 | AR392053 Sequence | |
| 9 | 933 | 67.7 | 933 | 6 | AR403913 | AR403913 Sequence | |
| 10 | 933 | 67.7 | 933 | 6 | AX320641 | AX320641 Sequence | |
| 11 | 932 | 67.6 | 932 | 6 | CQ731016 | CQ731016 Sequence | |
| 12 | 451 | 32.7 | 188646 | 9 | AC027045 | AC027045 Homo sapi | |

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query Match Length | DB | ID | Description |
|--------|-----|-------|-----------------------|-----|------------|--------------------|
| c | 1 | 621 | 45.0 | 631 | 1 AI091419 | AI091419 ow62e03.x |
| c | 2 | 551 | 40.0 | 632 | 1 AI741629 | AI741629 wg28f07.x |
| c | 3 | 495 | 35.9 | 562 | 1 AI458236 | AI458236 tj53e07.x |
| c | 4 | 485 | 35.2 | 632 | 1 AI741640 | AI741640 wg28g07.x |
| | 5 | 478 | 34.7 | 483 | 9 AY421548 | AY421548 Homo sapi |
| c | 6 | 473 | 34.3 | 473 | 1 AI376903 | AI376903 tc27f05.x |
| c | 7 | 469 | 34.0 | 469 | 1 AI141463 | AI141463 qa67d12.x |
| c | 8 | 414 | 30.0 | 558 | 1 AI222126 | AI222126 qh02g04.x |
| c | 9 | 261 | 18.9 | 505 | 1 AA953672 | AA953672 oo02e08.s |
| | 10 | 257 | 18.6 | 309 | 7 F26544 | F26544 HSPD14061 H |
| c | 11 | 256 | 18.6 | 307 | 1 AI470361 | AI470361 tj42f03.x |
| c | 12 | 254 | 18.4 | 477 | 1 AI168267 | AI168267 oo10c10.x |
| | 13 | 248 | 18.0 | 267 | 9 AY421549 | AY421549 Pan trogl |
| | 14 | 247 | 17.9 | 274 | 7 F35823 | F35823 HSPD32901 H |
| c | 15 | 243 | 17.6 | 396 | 1 AA928254 | AA928254 on79a08.s |
| c | 16 | 222 | 16.1 | 480 | 1 AI022337 | AI022337 ow95a11.x |